

CLUSTAL W (1.82) multiple sequence alignment

Searches / *29 = R* *arginine* *Page 1 of 1*
SwissProt Alignment

sp	P01555	CHTA_VIBCH	MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr	Q77DI6	Q77DI6_9VIRU	MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr	Q8VLI6	Q8VLI6_VIBCH	MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr	Q8L356	Q8L356_VIBCH	MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr	Q8LTG8	Q8LTG8_9VIRU	MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD
tr	Q6KE88	Q6KE88_VIBCH	MVKIIFVFFIFLSSFSYANDDKLYRADSRPPDEIKQSGGLMPRGQSEYFD

			1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
sp	P01555	CHTA_VIBCH	RGTQMNINLYDHARGTQTGFVRHDDGYVSTSI SLRSAHLVGQTILSGHST
tr	Q77DI6	Q77DI6_9VIRU	RGTQMNINLYDHARGTQTGFVRHDDGYVSTSI SLRSAHLVGQTILSGHST
tr	Q8VLI6	Q8VLI6_VIBCH	RGTQMNINLYDHARGTQTGFVRHDDGYVSTSI SLRSAHLVGQTILSGHST
tr	Q8L356	Q8L356_VIBCH	RGTQMNINLYDHARGTQTGFVRHDDGYVSTSI SLRSAHLVGQTILSGHST
tr	Q8LTG8	Q8LTG8_9VIRU	RGTQMNINLYDHARGTQTGFVRHDDGYVSTSI SLRSAHLVGQTILSGHST
tr	Q6KE88	Q6KE88_VIBCH	RGTQMNINLYDHARGTQTGFVRHDDGYVSTSI SLRSAHLVGQTILSGHST

sp	P01555	CHTA_VIBCH	YYIYVIATAPNMFNVNDVLGAYS PHPDEQEVSALGGIPYSQIYGWYRVHF
tr	Q77DI6	Q77DI6_9VIRU	YYIYVIATAPNMFNVNDVLGAYS PHPDEQEVSALGGIPYSQIYGWYRVHF
tr	Q8VLI6	Q8VLI6_VIBCH	YYIYVIATAPNMFNVNDVLGAYS PHPDEQEVSALGGIPYSQIYGWYRVHF
tr	Q8L356	Q8L356_VIBCH	YYIYVIATAPNMFNVNDVLGAYS PHPDEQEVSALGGIPYSQIYGWYRVHF
tr	Q8LTG8	Q8LTG8_9VIRU	YYIYVIATAPNMFNVNDVLGAYS PHPDEQEVSALGGIPYSQIYGWYRVHF
tr	Q6KE88	Q6KE88_VIBCH	YYIYVIATAPNMFNVNDVLGAYS PHPDEQEVSALGGIPYSQIYGWYRVHF

sp	P01555	CHTA_VIBCH	GVLDEQLHRNRYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIIHH
tr	Q77DI6	Q77DI6_9VIRU	GVLDEQLHRNRYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIIHH
tr	Q8VLI6	Q8VLI6_VIBCH	GVLDEQLHRNRYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIIHH
tr	Q8L356	Q8L356_VIBCH	GVLDEQLHRNRYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIIHH
tr	Q8LTG8	Q8LTG8_9VIRU	GVLDEQLHRNRYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIIHH
tr	Q6KE88	Q6KE88_VIBCH	GVLDEQLHRNRYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIIHH
			*****:*****:*****:*****:*****
sp	P01555	CHTA_VIBCH	APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr	Q77DI6	Q77DI6_9VIRU	APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr	Q8VLI6	Q8VLI6_VIBCH	APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr	Q8L356	Q8L356_VIBCH	APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr	Q8LTG8	Q8LTG8_9VIRU	APPGCGNAPRSSMSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDT
tr	Q6KE88	Q6KE88_VIBCH	PPPGCGNAPRSSMSNTCDEKPPQSLGVKFLDEYQSKVKRQIFSGYPSDIDT
			.*****.*****.*****.*****.*****
sp	P01555	CHTA_VIBCH	HNRIKDEL
tr	Q77DI6	Q77DI6_9VIRU	HNRIKDEL
tr	Q8VLI6	Q8VLI6_VIBCH	HNRIKDEL
tr	Q8L356	Q8L356_VIBCH	HNRIEDEL
tr	Q8LTG8	Q8LTG8_9VIRU	HNRIKDEL
tr	Q6KE88	Q6KE88_VIBCH	HNRIKDEL
			****:***

CLUSTAL W (1.82) multiple sequence alignment

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tr|Q57193|Q57193_VIBCH      MIKCLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q8LT24|Q8LT24_9VIRU     MIKCLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q9RP15|Q9RP15_VIBCH     MIKCLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q7B9N1|Q7B9N1_VIBCH     MIKCLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKILSYTE
tr|Q56635|Q56635_VIBCH     MIKCLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKILSYTE
tr|Q8LT25|Q8LT25_9VIRU     MIKCLKFGVFFTVLLSSAYAHGTPQNITDLWAEYHNTQIHTLNDKIFSYTE
sp|P01556|CHTB_VIBCH       MIKCLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDKIFSYTE
tr|Q77DH7|Q77DH7_9VIRU     MIKCLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDKIFSYTE
tr|Q8VLC4|Q8VLC4_VIBCH     MIKCLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q7BCC5|Q7BCC5_VIBCH     MIKCLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q94M01|Q94M01_9VIRU     MIKCLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q5Q031|Q5Q031_VIBCH     MIKCLKFGVFFIVLLSSAYAHGTPQNITDLCAEDHNTQIHTLNDKIFSYTE
sp|P13811|ELBH_ECOLI       MNKVKFYVLF TALLSSSLCAHGAPQSITELCSEYHNTQIYTINDKILSYTE
                               * *:*** *: * . ***** ***:*. ** * :* *****:*.****:****

tr|Q57193|Q57193_VIBCH     SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q8LT24|Q8LT24_9VIRU     SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q9RP15|Q9RP15_VIBCH     SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIDRMKDTRLRIAYLTE
tr|Q7B9N1|Q7B9N1_VIBCH     SLAGNREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q56635|Q56635_VIBCH     SLAGNREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q8LT25|Q8LT25_9VIRU     SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
sp|P01556|CHTB_VIBCH       SLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q77DH7|Q77DH7_9VIRU     SLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q8VLC4|Q8VLC4_VIBCH     SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q7BCC5|Q7BCC5_VIBCH     SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q94M01|Q94M01_9VIRU     SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q5Q031|Q5Q031_VIBCH     SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
sp|P13811|ELBH_ECOLI       SMAGKREMVIIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTRLITYLTE
                               *:***:***.*****. ** *****:*****:*****:****

tr|Q57193|Q57193_VIBCH     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8LT24|Q8LT24_9VIRU     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q9RP15|Q9RP15_VIBCH     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q7B9N1|Q7B9N1_VIBCH     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q56635|Q56635_VIBCH     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8LT25|Q8LT25_9VIRU     AKVEKLCVWNNKTPHAIAAISMAN
sp|P01556|CHTB_VIBCH       AKVEKLCVWNNKTPHAIAAISMAN
tr|Q77DH7|Q77DH7_9VIRU     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8VLC4|Q8VLC4_VIBCH     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q7BCC5|Q7BCC5_VIBCH     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q94M01|Q94M01_9VIRU     AKVEKLCVWNNKTPHAIAAISMAN
tr|Q5Q031|Q5Q031_VIBCH     AKVEKLCVWNNKTPHAIAAISMAN
sp|P13811|ELBH_ECOLI       TKIDKLCVWNNKTPNSIAAISMAN
                               *:*****:***** *

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CLUSTAL W (1.82) multiple sequence alignment

```

tr|Q57193|Q57193_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q8LT24|Q8LT24_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q9RP15|Q9RP15_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKIFSYTE
tr|Q7B9N1|Q7B9N1_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKILSYTE
tr|Q56635|Q56635_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIHTLNDKILSYTE
tr|Q8LT25|Q8LT25_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPQNITDLWAEYHNTQIHTLNDKIFSYTE
sp|P01556|CHTB_VIBCH        MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDKIFSYTE
tr|Q77DH7|Q77DH7_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPQNITDLCAEYHNTQIYTLNDKIFSYTE
tr|Q8VLC4|Q8VLC4_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q7BCC5|Q7BCC5_VIBCH      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q94M01|Q94M01_9VIRU      MIKLKFGVFFTVLLSSAYAHGTPHNITALCAEYHNTQIHTLNDKIFSYTE
tr|Q5Q031|Q5Q031_VIBCH      MIKLKFGVFFIVLLSSAYAHGTPQNITDLCAEDHNTQIHTLNDKIFSYTE
*****:*** * ** *****:*****:****

tr|Q57193|Q57193_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q8LT24|Q8LT24_9VIRU      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q9RP15|Q9RP15_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIDRMKDTRLRIAYLTE
tr|Q7B9N1|Q7B9N1_VIBCH      SLAGNREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q56635|Q56635_VIBCH      SLAGNREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q8LT25|Q8LT25_9VIRU      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
sp|P01556|CHTB_VIBCH        SLAGKREMAIITFKNGAIFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
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tr|Q8VLC4|Q8VLC4_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q7BCC5|Q7BCC5_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q94M01|Q94M01_9VIRU      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
tr|Q5Q031|Q5Q031_VIBCH      SLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTRLRIAYLTE
****:***** *****:*****

tr|Q57193|Q57193_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8LT24|Q8LT24_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q9RP15|Q9RP15_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q7B9N1|Q7B9N1_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q56635|Q56635_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8LT25|Q8LT25_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
sp|P01556|CHTB_VIBCH        AKVEKLCVWNNKTPHAIAAISMAN
tr|Q77DH7|Q77DH7_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q8VLC4|Q8VLC4_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q7BCC5|Q7BCC5_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q94M01|Q94M01_9VIRU      AKVEKLCVWNNKTPHAIAAISMAN
tr|Q5Q031|Q5Q031_VIBCH      AKVEKLCVWNNKTPHAIAAISMAN
*****

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Entry information

Entry name	E2BB_ECOLI
Primary accession number	P43529
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 32, November 1995
Sequence was last modified in	Release 32, November 1995
Annotations were last modified in	Release 49, January 2006
Name and origin of the protein	
Protein name	Heat-labile enterotoxin IIB, B chain [Precursor]
Synonym	LT-IIB
Gene name	None
From	Escherichia coli [TaxID: 562]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=Isolate 41;

PubMed=2670900 [NCBI, ExPASy, EBI, Israel, Japan]

Pickett C.L., Twiddy E.M., Coker C., Holmes R.K.;

"Cloning, nucleotide sequence, and hybridization studies of the type IIB heat-labile enterotoxin gene of Escherichia coli.";

J. Bacteriol. 171:4945-4952(1989).

[2] X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).

DOI=10.1016/S0969-2126(96)00073-1; PubMed=8805549 [NCBI, ExPASy, EBI, Israel, Japan]

van den Akker F., Sarfaty S., Twiddy E.M., Connell T.D., Holmes R.K., Hol W.G.J.;

"Crystal structure of a new heat-labile enterotoxin, LT-IIB.";

Structure 4:665-678(1996).

Comments

- **FUNCTION:** The biological activity of the toxin is produced by the A chain, which activates intracellular adenyl cyclase.
- **SUBUNIT:** Heterohexamer of one A chain and of five B chains.

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Cross-references

EMBL M28523; AAA53286.1; -; [EMBL / GenBank / DDBJ]
 Genomic_DNA. [CoDingSequence]

PIR B33959; B33959.

PDB 1QB5; X-ray; D/E/F/G/H=24-122. [ExPASy / RCSB / EBI]
 1QCB; X-ray; D/E/F/G/H=24-122. [ExPASy / RCSB / EBI]
 1TII; X-ray; D/E/F/G/H=24-122. [ExPASy / RCSB / EBI]
 Detailed list of linked structures.

InterPro IPR010503; LT-IIB.
 Graphical view of domain structure.

Pfam PF06453; LT-IIB; 1.
 Pfam graphical view of domain structure.

ProDom PD031532; LT-IIB; 1.
 [Domain structure / List of seq. sharing at least 1 domain]

HOGENOM [Family / Alignment / Tree]

BLOCKS P43529.

ProtoNet P43529.

ProtoMap P43529.

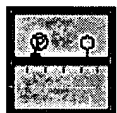
PRESAGE P43529.

DIP P43529.

ModBase P43529.

SWISS-2DPAGE Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords**3D-structure; Enterotoxin; Signal; Toxin.****Features**

Feature table viewer

Key	From	To	Length	Description	FTId
SIGNAL	1	23	23		
CHAIN	24	122	99	Heat-labile enterotoxin IIB, B chain.	PRO_0000019358
DISULFID	33	104			
HELIX	27	33	7		
TURN	34	35	2		
STRAND	39	44	6		
STRAND	46	52	7		
TURN	55	57	3		
STRAND	59	64	6		
TURN	65	66	2		
STRAND	69	72	4		
TURN	78	79	2		
HELIX	80	97	18		
STRAND	101	106	6		
TURN	107	108	2		
STRAND	112	120	9		

Sequence information

Length: **122 AA** [This is the length of the unprocessed precursor] Molecular weight: **13255 Da** [This is the MW of the unprocessed precursor] CRC64: **308A6CE5F0CFD494** [This is a checksum on the sequence]

```

      10      20      30      40      50      60
MSFKKIIKAF VIMAALVSVQ AHAGASQFFK DNCNRTTASL VEGVELTKYI SDINNNTDGM

      70      80      90     100     110     120
YVVSSTGGVW RISRAKDYPD NVMTAEMRKI AMAAVLSGMR VNCASPASS PNVIWAIELE

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AE

P43529 in FASTA format

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or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-
MODEL



NPSA Sequence analysis
tools



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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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Entry information

Entry name **CHTA_VIBCH**Primary accession number **P01555**Secondary accession numbers **Q56634 Q9JPV1**Entered in Swiss-Prot in **Release 01, July 1986**Sequence was last modified in **Release 02, October 1986**Annotations were last modified in **Release 49, January 2006**

Name and origin of the protein

Protein name **Cholera enterotoxin, A chain [Precursor]**Synonyms **NAD(+)--diphthamide ADP-ribosyltransferase
EC 2.4.2.36****Cholera enterotoxin A subunit****Cholera enterotoxin subunit A1**

(Cholera enterotoxin A1 chain)

(Cholera enterotoxin alpha chain)

Contains

Cholera enterotoxin subunit A2

(Cholera enterotoxin A2 chain)

(Cholera enterotoxin gamma chain)

Gene name

Name: ctxA

Synonyms: toxA

OrderedLocusNames: VC1457

From

Vibrio cholerae [TaxID: 666]

Taxonomy

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=El Tor 2125;

PubMed=6646234 [NCBI, ExPASy, EBI, Israel, Japan]

Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F., de Wilde M.;

"Cholera toxin genes: nucleotide sequence, deletion analysis and vaccine development.";

Nature 306:551-557(1983).

[2]


NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=Classical 569B / ATCC 25870 / Serotype O1;

DOI=10.1016/0167-4781(91)90050-V; PubMed=1883840 [NCBI, ExPASy, EBI, Israel, Japan]

Dams E., de Wolf M., Dierick W.;

"Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classical strain 569B.";

- Biochim. Biophys. Acta 1090:139-141(1991).
- [3] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=1854 / O139-Bengal;
Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J., Honda T.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
- [4] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=El Tor 2125;
Dams E., de Wolf M., Dierick W.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
- [5] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=KNIH002;
Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nucleotide sequence analysis of the virulence gene cassette from *Vibrio cholerae* KNIH002 isolated in Korea.";
Misainmurhag Hoiiji 35:205-210(1999).
- [6] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=El Tor N16961 / Serotype O1;
DOI=10.1038/35020000; PubMed=10952301 [NCBI, ExPASy, EBI, Israel, Japan]
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L., Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., , Fraser C.M.;
"DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.";
Nature 406:477-483(2000).
- [7] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-212.
STRAIN=Classical 569B / ATCC 25870 / Serotype O1;
PubMed=6090390 [NCBI, ExPASy, EBI, Israel, Japan]
Lockman H.A., Galen J.E., Kaper J.B.;
"Vibrio cholerae enterotoxin genes: nucleotide sequence analysis of DNA encoding ADP-ribosyltransferase.";
J. Bacteriol. 159:1086-1089(1984).
- [8] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 213-258.
PubMed=6315707 [NCBI, ExPASy, EBI, Israel, Japan]
Lockman H., Kaper J.B.;
"Nucleotide sequence analysis of the A2 and B subunits of *Vibrio cholerae* enterotoxin.";
J. Biol. Chem. 258:13722-13726(1983).
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Zhang R.-G., Scott D.L., Westbrook M.L., Nance S., Spangler B.D., Shipley G.G., Westbrook
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Comments

- **FUNCTION:** The A1 chain catalyzes the ADP-ribosylation of Gs alpha, a GTP-binding regulatory protein, to activate the adenylate cyclase. This leads to an overproduction of cAMP and eventually to a hypersecretion of chloride and bicarbonate followed by water, resulting in the characteristic cholera stool. The A2 chain tethers A1 to the pentameric ring.
- **CATALYTIC ACTIVITY:** NAD^+ + peptide diphthamide = nicotinamide + peptide N-(ADP-D-ribose)diphthamide.
- **SUBUNIT:** The holotoxin (cholera toxin) consists of a pentameric ring of B subunits whose central pore is occupied by the A subunit. The A subunit contains two chains, A1 and A2, linked by a disulfide bridge.
- **DOMAIN:** The four C-terminal residues of the A2 chain occupy the central pore of the holotoxin. Deletion of these residues weakens the interaction between the A subunit and the B pentamer without impairing the pentamer formation.
- **MISCELLANEOUS:** After binding to gangliosides GM1 in lipid rafts, through the subunit B pentamer, the holotoxin and the gangliosides are internalized. The holotoxin remains bound to GM1 until arrival in the ER. The A subunit has previously been cleaved in the intestinal lumen but the A1 and A2 chains have remained associated. In the ER, the A subunit disulfide bridge is reduced, the A1 chain is unfolded by the PDI and disassembled from the rest of the toxin. Then, the membrane-associated ER oxidase ERO1 oxidizes PDI, which releases the unfolded A1 chain.

The next step is the retro-translocation of A1 into the cytosol. This might be mediated by the protein-conducting pore SEC61. Upon arrival in the cytosol, A1 refolds and avoids proteasome degradation. In one way or another, A1 finally reaches its target and induces toxicity.

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Cross-references

EMBL	X00171; CAA24995.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	X58785; CAA41590.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	D30053; BAA06290.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	X58786; CAA41592.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	K02679; AAA27514.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	AF175708; AAD51359.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	AE004224; AAF94614.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
PIR	K01170; AAA27572.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
PIR	D30052; BAA06288.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
PDB	A05129; XVVCA.	
	1S5B; X-ray; A=19-258.	[ExPASy / RCSB / EBI]
	1S5C; X-ray; A=19-258.	[ExPASy / RCSB / EBI]
	1S5D; X-ray; A=19-258.	[ExPASy / RCSB / EBI]
	1S5E; X-ray; A/B=19-258.	[ExPASy / RCSB / EBI]
	1S5F; X-ray; A=19-258.	[ExPASy / RCSB / EBI]
TIGR	1XTC; X-ray; A=19-212, C=213-258.	[ExPASy / RCSB / EBI]
	Detailed list of linked structures.	
InterPro	VC1457; -.	
	IPR001144; Enterotoxin_A.	
Pfam	Graphical view of domain structure.	
	PF01375; Enterotoxin_a; 1.	
PRINTS	Pfam graphical view of domain structure.	
	PR00771; ENTEROTOXINA.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGENOM	[Family / Alignment / Tree]	
BLOCKS	P01555.	
ProtoNet	P01555.	
ProtoMap	P01555.	
PRESAGE	P01555.	
DIP	P01555.	
ModBase	P01555.	

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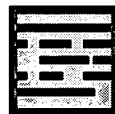
Keywords

3D-structure; Complete proteome; Direct protein sequencing; Enterotoxin; Glycosyltransferase; NAD; Signal; Toxin; Transferase.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FTId
SIGNAL	1	18	18		
CHAIN	19	212	194	Cholera enterotoxin subunit A1.	PRO_0000019342
CHAIN	213	258	46	Cholera enterotoxin subunit A2.	PRO_0000019343
ACT_SITE	130	130		By similarity.	
BINDING	25	25		NAD (By similarity).	
BINDING	62	62		NAD (By similarity).	
DISULFID	205	217		Interchain (between A1 and A2 chains).	
CONFLICT	20	20		D -> N (in Ref. 9).	
CONFLICT	37	37		S -> R (in Ref. 10).	
CONFLICT	39	39		G -> L (in Ref. 11).	
CONFLICT	45	46		QS -> SE (in Ref. 11).	
CONFLICT	111	111		N -> L (in Ref. 11).	
CONFLICT	132	132		S -> A (in Ref. 11).	
CONFLICT	213	213		M -> I (in Ref. 1).	
CONFLICT	247	248		DI -> ID (in Ref. 12).	
CONFLICT	256	256		D -> N (in Ref. 12).	
STRAND	24	27	4		
HELIX	31	37	7		
TURN	38	38	1		
STRAND	39	40	2		
TURN	43	44	2		
TURN	48	49	2		
HELIX	59	63	5		
TURN	64	64	1		
TURN	75	76	2		
STRAND	77	81	5		
HELIX	85	89	5		
TURN	90	91	2		
TURN	96	97	2		
STRAND	101	106	6		
TURN	110	111	2		
STRAND	112	114	3		
HELIX	115	119	5		
HELIX	120	122	3		
HELIX	126	128	3		
STRAND	130	134	5		

STRAND	137	138	2
TURN	139	141	3
STRAND	142	148	7
STRAND	153	159	7
TURN	161	162	2
HELIX	165	168	4
TURN	169	170	2
HELIX	176	178	3
TURN	187	188	2
HELIX	190	193	4
TURN	195	196	2
HELIX	197	199	3
TURN	200	200	1
TURN	203	204	2
HELIX	215	251	37
TURN	252	253	2
HELIX	254	258	5

Sequence information

Length: **258 AA** [This is the length of the unprocessed precursor]

Molecular weight: **29336 Da** [This is the MW of the unprocessed precursor]

CRC64: **0F7EBAE62069A5D0** [This is a checksum on the sequence]

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MVKIIFVFFI	FLSSFSYAND	DKLYRADSRP	PDEIKQSGGL	MPRGQSEYFD	RGTQMNINLY
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
DHARGTQTGF	VRHDDGYVST	SISLRSAHLV	GQTILSGHST	YYIYVIATAP	NMFNVNDVLG
<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
AYSPPHDEQE	VSALGGIPYS	QIYGWYRVHF	GVLDEQLHRN	RGYRDRYYSN	LDIAPAADGY
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
GLAGFPPEHR	AWREEPWIIH	APPGCGNAPR	SSMSNTCDEK	TQSLGVKFLD	EYQSKVKRQI
<u>250</u>					
FSGYQSDIDT	HNRIKDEL				

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